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Search	Most Recent Queries	Time	Result
#38	Search **Kluyveromyces AND reductase** Field: **Title/Abstract**	16:15:47	9
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#33	Search **enone reductase** Field: **Title/Abstract**	16:14:28	4
#32	Search **Kluyveromyces AND enzyme AND (enone or ketone or carbon)** Field: **Title/Abstract**	16:13:50	15
#31	Search **Kluyveromyces AND reductase AND (enone or ketone or carbon)** Field: **Title/Abstract**	16:13:20	0

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Jan 29 2004 15:06:34

NCBI results of BLAST

BLASTP 2.2.8 [Jan-05-2004]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1076620068-13214-9170067263.BLASTQ3

Query=
(118 letters)

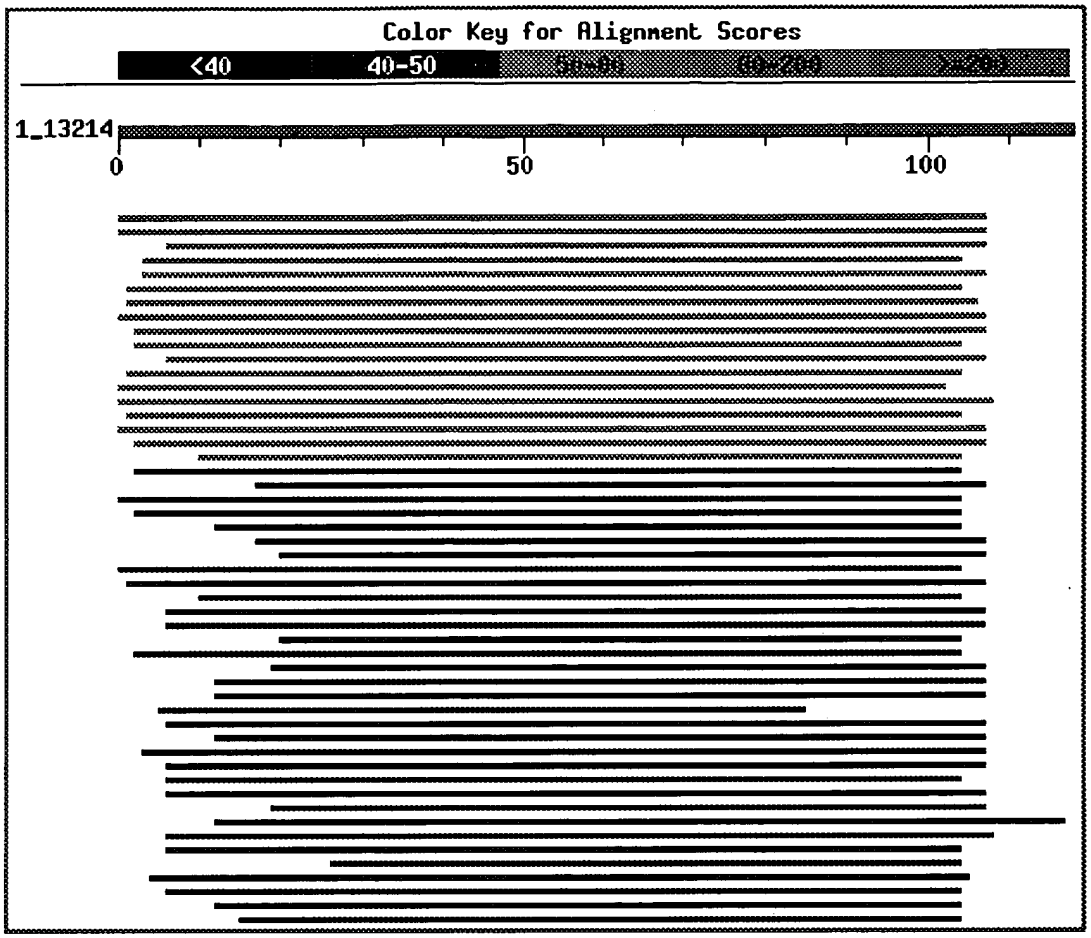
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
1,643,721 sequences; 539,141,899 total letters

If you have any problems or questions with the results of this search please refer to the **BLAST FAQs**

Taxonomy reports

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:		Score (bits)	E Value
gi|6324195|ref|NP_014265.1|	Ynl134cp [Saccharomyces cerevis...	135	1e-31
gi|6323493|ref|NP_013565.1|	Hypothetical ORF; Ylr460cp [Sac...	134	3e-31
gi|6319945|ref|NP_010026.1|	Hypothetical ORF; Ycr102cp [Sac...	127	4e-29
gi|40741495|gb|EAA60685.1|	hypothetical protein AN8651.2 [A...	96	1e-19
gi|1729996|sp|P54006|TOXD_COCCA	TOXD protein >gi|1027511|em...	77	7e-14
gi|38111915|gb|EAA57410.1|	hypothetical protein MG08380.4 [...	68	3e-11
gi|38111928|gb|EAA57421.1|	hypothetical protein MG08391.4 [...	63	1e-09
gi|38106089|gb|EAA52440.1|	hypothetical protein MG05132.4 [...	61	3e-09
gi|40747875|gb|EAA67031.1|	hypothetical protein AN8409.2 [A...	59	2e-08
gi|38105395|gb|EAA51829.1|	hypothetical protein MG03424.4 [...	57	5e-08

Alignments

Get selected sequences | Select all | Deselect all

☐ >gi|6324195|ref|NP_014265.1| Ynl134cp [Saccharomyces cerevisiae]
gi|1730779|sp|P53912|YNN4_YEAST HYPOTHETICAL 41.2 KD PROTEIN IN FPR1-TOM22 INTERG
gi|1078063|pir||S55149 hypothetical protein YNL134c - yeast (Saccharomyces cerevi
gi|854503|emb|CAA86891.1| orf14 [Saccharomyces cerevisiae]
gi|1302076|emb|CAA96016.1| unnamed protein product [Saccharomyces cerevisiae]

Length = 376

Score = 135 bits (341), Expect = 1e-31
Identities = 65/109 (59%), Positives = 82/109 (75%), Gaps = 1/109 (0%)

```
Query: 1   SVPTTQKAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSIL 60
           S+P T KAV+IE  KAVVK D+ +PEL+EG  L+K  AVAGNPTDWKHI +KIGP+G++L
Sbjct: 4   SIPETMKAVVIENGKAVVKQDIPIPELEEGFVLIKTVAVAGNPTDWKHIDFKIGPQGALL 63

Query: 61  GCDIAGTVVKLGPNA-STDLKVGDTGFGFVHGASQTDPKNGAFAEYARV 108
           GCD AG +VKLGPN  +    +GD  +G +HGAS   P NGAFAEY+ +
Sbjct: 64  GCDAAGQIVKLGPNVDAARFAIGDYIYGVIHGASVRFPSNGAFAEYSAI 112
```

>gi|6323493|ref|NP_013565.1| Hypothetical ORF; Ylr460cp [Saccharomyces cerevisia
gi|1730591|sp|P54007|YL60_YEAST Hypothetical 41.1 kDa protein ON CDC91-PAU4 inter
gi|1363734|pir||S59418 hypothetical protein YLR460c - yeast (Saccharomyces cerevi
gi|717077|gb|AAB64723.1| Ylr460cp [Saccharomyces cerevisiae]
Length = 376

Score = 134 bits (337), Expect = 3e-31
Identities = 65/109 (59%), Positives = 81/109 (74%), Gaps = 1/109 (0%)

```
Query: 1   SVPTTQKAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSIL 60
           ++P T KAV+IE  KAVVK  + +PEL+EG  L+K  AVAGNPTDW HI YKIGP+GSIL
Sbjct: 4   AIPETMKAVVIEDGKAVVKEGIPIPELEEGFVLIKTLAVAGNPTDWAHIDYKIGPQGSIL 63

Query: 61  GCDIAGTVVKLGPNAS-TDLKVGDTGFGFVHGASQTDPKNGAFAEYARV 108
           GCD AG +VKLGP  +  D  +GD  +GF+HG+S   P NGAFAEY+ +
Sbjct: 64  GCDAAGQIVKLGPAVNPKDFSIGDYIYGFIHGSSVRFPSNGAFAEYSAI 112
```

>gi|6319945|ref|NP_010026.1| Hypothetical ORF; Ycr102cp [Saccharomyces cerevisia
gi|140561|sp|P25608|YCZ2_YEAST 40.1 KD PROTEIN IN GIT1-PAU3 INTERGENIC REGION
gi|83274|pir||S19414 hypothetical protein YCR102c - yeast (Saccharomyces cerevisi
gi|1907240|emb|CAA42244.1| hypothetical protein [Saccharomyces cerevisiae]
Length = 368

Score = 127 bits (319), Expect = 4e-29
Identities = 63/103 (61%), Positives = 76/103 (73%), Gaps = 1/103 (0%)

```
Query: 7   KAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSILGCDIAG 66
           KAV+IE  KAVVK  V +PEL+EG  L+K  AVAGNPTDW HI YK+GP+GSILGCD AG
Sbjct: 2   KAVVIEDGKAVVKEGVPIPELEEGFVLIKTLAVAGNPTDWAHIDYKVGPQGSILGCDAAG 61

Query: 67  TVVKLGPNAS-TDLKVGDTGFGFVHGASQTDPKNGAFAEYARV 108
            +VKLGP     D  +GD  +GF+HG+S   P NGAFAEY+ +
Sbjct: 62  QIVKLGPAVDPKDFSIGDYIYGFIHGSSVRFPSNGAFAEYSAI 104
```

>gi|40741495|gb|EAA60685.1| hypothetical protein AN8651.2 [Aspergillus nidulans
Length = 566

Score = 95.9 bits (237), Expect = 1e-19
Identities = 52/103 (50%), Positives = 68/103 (66%), Gaps = 2/103 (1%)

```
Query: 4   TTQKAVIIEGDK-AVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSILGC 62
           +TQKAV+I    K    + TD  +P L++    LVK  AVA NPTDWKHIAY + P G ++GC
Sbjct: 2   STQKAVVITSPKQGGLVTDRPIPALRDDYILVKNVAVALNPTDWKHIAY-LAPPGVLVGC 60

Query: 63  DIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEY 105
           D AG V ++G N      K GD    GF+HG++Q   P++GAFAEY
Sbjct: 61  DYAGIVEEVGKNVKKPFKKGDRIAGFIHGSNQVQPEDGAFAEY 103
```

>gi|1729996|sp|P54006|TOXD_COCCA TOXD protein
gi|1027511|emb|CAA63129.1| toxD [Cochliobolus carbonum]
Length = 297

Score = 76.6 bits (187), Expect = 7e-14
Identities = 42/106 (39%), Positives = 62/106 (58%), Gaps = 2/106 (1%)

```
Query: 4   TTQKAVIIEG-DKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSILGC 62
           T QKA++ E    +A + +D  +P+L++    LV+  +VA NPTDWKHI  ++ P G ++GC
Sbjct: 2   TFQKAIVTEAPHRARLVSDRLIPKLRDDYILVRTVSVALNPTDWKHI-LRLSPPGCLVGC 60

Query: 63  DIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARV 108
           D AG V ++G +      K GD    GF HG +      +G FAE   V
Sbjct: 61  DYAGIVEEVGRSVKKPFKKGDRVCGFAHGGNAVFSDDGTFAEVITV 106
```

>gi|38111915|gb|EAA57410.1| hypothetical protein MG08380.4 [Magnaporthe grisea 7
Length = 353

Score = 68.2 bits (165), Expect = 3e-11
Identities = 43/107 (40%), Positives = 66/107 (61%), Gaps = 7/107 (6%)

```
Query: 2   VPTTQKAVIIEGDKAVVKTD--VSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPE-GS 58
           +P+ + A I++ DK  +K D     +P+ +     LV+V+AVA NP D  H  Y+  P  G+
Sbjct: 3   IPSARTA-IVQDDKGGLKIDRNAPMPQPRPNELLVQVKAVAINPCD--HKMYERFPTPGA 59

Query: 59  ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEY 105
           + GCD AG VV+LG +  T   ++GD    G VHG++  + P++G FAEY
Sbjct: 60  VDGCDFAGIVVQLGSDVKT-FQIGDRVCGAVHGSNPSRPESGTFAEY 105
```

>gi|38111928|gb|EAA57421.1| hypothetical protein MG08391.4 [Magnaporthe grisea 7
Length = 400

Score = 62.8 bits (151), Expect = 1e-09
Identities = 42/110 (38%), Positives = 59/110 (53%), Gaps = 5/110 (4%)

```
Query: 2   VPTTQKAVIIEGDKAVVKTD--VSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSI 59
           +P++  A+I    D   VK     + +P L+ G  LVK  AVA NP D+K +  +    G+
Sbjct: 46  IPSSHTAIIQHDDAGGVKITPGLPLPVLEPGQVLVKTAAVALNPCDFK-MPQRFSQAGTY 104

Query: 60  LGCDIAGTVVKLGPNASTD--LKVGDTGFGFVHGASQTDPKNGAFAEYAR 107
            GCD AGTVV+L      +  LKVGD   F    G +  D  +G+FAEY +
Sbjct: 105 NGCDYAGTVVQLTEEVEKNGLLKVGDRIFAACVGNNPHDKDSGSFAEYLK 154
```

>gi|38106089|gb|EAA52440.1| hypothetical protein MG05132.4 [Magnaporthe grisea
Length = 361

Score = 61.2 bits (147), Expect = 3e-09
Identities = 42/111 (37%), Positives = 61/111 (54%), Gaps = 7/111 (6%)

```
Query: 1   SVPTTQKAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAY---KIGPEG 57
           ++P+  +A+I       V    V  P+L++   LVK  AVA NPT+  H  +    + P G
Sbjct: 2   AIPSKARALIKTQKGKVEVQTVPTPKLRDNYVLVKTTAVALNPTE-PHAVFDDDTVQP-G 59

Query: 58  SILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARV 108
           S++GCD AG VV+ G N+    K GD   G  HG +  + ++GAFAEY  V
Sbjct: 60  SLVGCDFAGVVVEAGDNSR--FKPGDRIAGMAHGGNAENMEDGAFAEYINV 108
```

>gi|40747875|gb|EAA67031.1| hypothetical protein AN8409.2 [Aspergillus nidulans
Length = 333

Score = 58.5 bits (140), Expect = 2e-08
Identities = 39/108 (36%), Positives = 57/108 (52%), Gaps = 4/108 (3%)

```
Query: 3   PTTQKAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPE-GSILG 61
           P  Q A+ I  +  +       +P L++   LV V+++A NP D K  + ++ P  G+ LG
Sbjct: 4   PKQQTALKITPEGRIAAVSSPLPSLQDNELLVCVKSIALNPFDAK--SAEMSPTIGATLG 61

Query: 62  CDIAGTVVKLGPNAST-DLKVGDTGFGFVHGASQTDPKNGAFAEYARV 108
           CD AG +V  G NA+  +  +GD   G V G +     NGAFAEY  V
Sbjct: 62  CDFAGKIVATGSNANDFNFSIGDRVCGCVFGNNPNRLDNGAFAEYVAV 109
```

>gi|38105395|gb|EAA51829.1| hypothetical protein MG03424.4 [Magnaporthe grisea
Length = 350

Score = 57.4 bits (137), Expect = 5e-08
Identities = 40/104 (38%), Positives = 54/104 (51%), Gaps = 3/104 (2%)

```
Query: 3   PTTQKAVII-EGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSILG 61
           P TQ  +++ E D  VV+ D   P L     LV+V AV  NP+D K       P+ +ILG
Sbjct: 6   PATQPGLVVDEHDNVVVRADCPFPSLPADQVLVRVRAVGVNPSDTKMRGPFALPQ-AILG 64

Query: 62  CDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEY 105
            D AG VV +G     D+ VGD   G  +  + +P+ GAFA Y
Sbjct: 65  ADFAGDVVAVGAEVR-DVAVGDRVCGAQNELFRPEPERGAFAAY 107
```

Get selected sequences | Select all | Deselect all

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
Posted date: Feb 11, 2004 6:26 AM
Number of letters in database: 539,141,899
Number of sequences in database: 1,643,721

```
Lambda      K       H
   0.312    0.134    0.388

Gapped
Lambda      K       H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 13,287,786
Number of Sequences: 1643721
Number of extensions: 518145
Number of successful extensions: 879
Number of sequences better than 10.0: 30
Number of HSP's better than 10.0 without gapping: 7
Number of HSP's successfully gapped in prelim test: 23
Number of HSP's that attempted gapping in prelim test: 863
Number of HSP's gapped (non-prelim): 31
length of query: 118
length of database: 539,141,899
effective HSP length: 94
effective length of query: 24
effective length of database: 384,632,125
effective search space: 9231171000
effective search space used: 9231171000
T: 11
A: 40
X1: 16 ( 7.2 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (21.8 bits)
S2: 66 (30.0 bits)
```

WEST Search History

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DATE: Thursday, February 12, 2004

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR		
☐	L6	alpha-beta-unsaturated adj ketone$2 with (reduc$5 or break or cleav$ or enzym$)	2
☐	L5	alpha-beta-unsaturated adj ketone$2 and nadph	1
☐	L4	alpha-beta-unsaturated adj ketones and nadph	1
☐	L3	alpha-beta-unsaturated ketones and nadph	1917
☐	L2	alpha-beta-unsaturated adj ketones with (reduc$5 or break or cleav$ or enzym$)	2
☐	L1	enone adj reductase	8

END OF SEARCH HISTORY